

## AMENDMENTS

### Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

### Listing of Claims:

1. (previously presented) A method for determining coat colour genotype in a pig which comprises:

(a) obtaining a sample of pig nucleic acid; and

(b) analysing the nucleic acid obtained in (a) to determine whether a mutation is/is not present at an exon 17/intron 17 splice site of a KIT gene, wherein the mutation consists of the substitution of the G in the conserved GT pair by A.

2. (canceled)

3. (canceled)

4. (**currently amended**) The method according to claim 1 ~~or 3~~, wherein the sample of nucleic acid is amplified prior to analysis.

5. (previously presented) The method according to claim 4, wherein the nucleic acid is genomic DNA.

6. (previously presented) The method according to claim 5, wherein amplification is carried out using PCR and at least one pair of suitable primers.

7. (previously presented) The method according to claim 6, wherein the pair of suitable primers is:

5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ. ID No. 1); and

5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ. ID No. 2).

8. (previously presented) The method according to claim 5, wherein after amplification the nucleic acid is treated with a restriction enzyme, followed by analysis of fragment lengths.
9. (previously presented) The method according to claim 8, wherein the nucleic acid is treated with the restriction enzyme *NlaIII*.
10. (previously presented) The method according to claim 8, wherein the ratio of restriction fragment lengths is determined.
11. (previously presented) The method according to claim 4, wherein the nucleic acid is mRNA.
12. (previously presented) The method according to claim 11, wherein the nucleic acid is amplified using RT-PCR.
13. (previously presented) The method according to claim 12, wherein the length of RT-PCR product is determined.
14. (previously presented) A method for determining coat colour genotype in a pig which comprises the step of analysing a sample of pig KIT protein to determine whether the protein is a splice variant protein produced by the substitution of G in the conserved GT pair by A, at an exon 17/intron 17 splice site of a KIT gene, said splice variant protein being correlated with coat colour genotype.
15. (previously presented) A kit for use in determining the coat colour genotype of a pig which comprises one or more reagents for carrying out PCR and the following pair of primers:  
5'-GTA TTC ACA GAG ACT TGG CGG C-3' (SEQ ID No. 1);  
5'-AAA CCT GCA AGG AAA ATC CTT CAC GG-3' (SEQ ID No. 2).

16. (canceled)

17. (canceled)

18. (previously presented) The method of claim 1, wherein the presence or absence of said mutation is determined in each copy of the KIT gene in the pig's genome, and the ratio of the number of KIT genes lacking the mutation to the number of KIT genes containing the mutation is determined.

19. (previously presented) The method according to claim 9, wherein the ratio of restriction fragment lengths is determined.